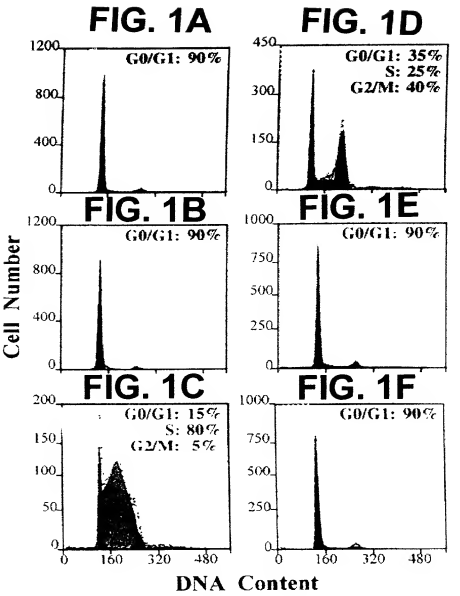
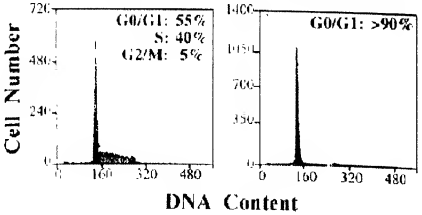


FIG. 1A
G0/G1: 90%
1200
800
400
0
FIG. 1D
G0/G1: 35%
S: 25%
G2/M: 40%
450
300
150
0
FIG. 1B
G0/G1: 90%
1200
800
400
0
FIG. 1E
G0/G1: 90%
1000
750
500
250
0
Cell Number
FIG. 1C
G0/G1: 15%
S: 80%
G2/M: 5%
200
150
100
50
0
0 160 320 480
FIG. 1F
G0/G1: 90%
1000
750
500
250
0
0 160 320 480
DNA Content

FIG. 1G

FIG. 2A

FIG. 2B



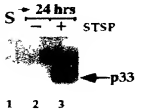


FIG. 2C

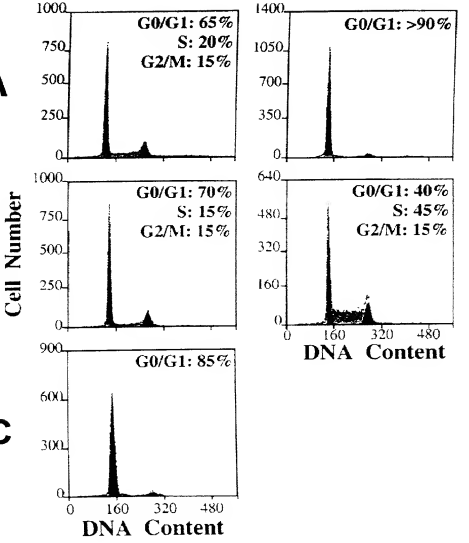


FIG. 3A

FIG. 3D

FIG. 3B

FIG. 3E

FIG. 3C

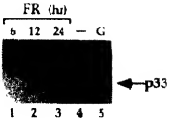


FIG. 3F

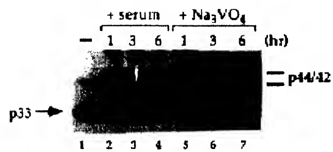


FIG. 4

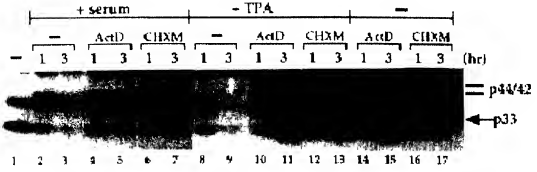


FIG. 5

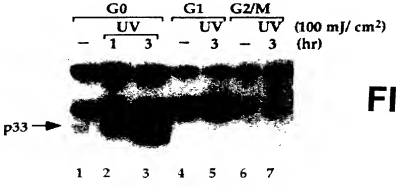


FIG. 6A

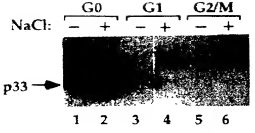


FIG. 6B

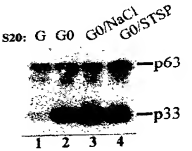


FIG. 7A

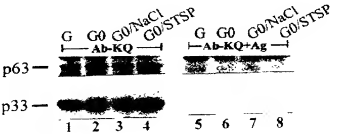


FIG. 7B

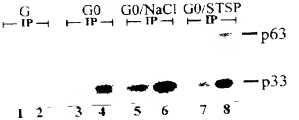


FIG. 7C

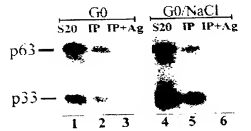


FIG. 7D

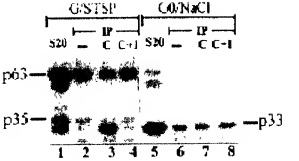


FIG. 8

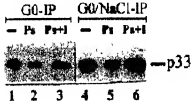


FIG. 9

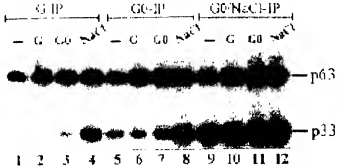


FIG. 10

Human p63Krs1/SAMK gene and encoded sequence

```
   1.  atggagcagccgccggcgcctaagagtaaactaaaaaagctgagtgaagacagtttgactaagcagcctgaagaa
   1.  M  E  Q  P  P  A  P  K  S  K  L  K  K  L  S  E  D  S  L  T  K  Q  P  E  E

  76.  gtttttgatgtattagagaagcttggagaagggtcttatggaagtgtatttaaagcaatacacaaggaatccggt
  26.  V  F  D  V  L  E  K  L  G  E  G  S  Y  G  S  V  F  K  A  I  H  K  E  S  G

 151.  caagttgtcgcaattaaacaagtacctgttgaatcagatcttcaggaaataatcaaagaaatttccataatgcag
  51.  Q  V  V  A  I  K  Q  V  P  V  E  S  D  L  Q  E  I  I  K  E  I  S  I  M  Q

 226.  caatgtgacagccatatgttgtaaagtactatggcagttattttaagaatacagacctctggattgttatggag
  76.  Q  C  D  S  P  Y  V  V  K  Y  Y  G  S  Y  F  K  N  T  D  L  W  I  V  M  E

 301.  tactgtggcgctggctctgtctcagacataattagattacgaaacaagacattaatagaagatgaaattgcaacc
 101.  Y  C  G  A  G  S  V  S  D  I  I  R  L  R  N  K  T  L  I  E  D  E  I  A  T

 376.  attcttaaatctacattgaaaggactagaatatttgcacttttatgagaaaaatacacagagatataaaagctgga
 126.  I  L  K  S  T  L  K  G  L  E  Y  L  H  F  M  R  K  I  H  R  D  I  K  A  G

 451.  aatattctcctcaatacagaaggacatgcaaaattggcagattttggagtggctggtcagttaacagatacaatg
 151.  N  I  L  L  N  T  E  G  H  A  K  L  A  D  F  G  V  A  G  Q  L  T  D  T  M

 526.  gcaaaacgcaatactgtaataggaactccattttggatggctcctgaggtgattcaagaaataggctatactgt
 176.  A  K  R  N  T  V  I  G  T  P  F  W  M  A  P  E  V  I  Q  E  I  G  Y  N  C

 601.  gtggccgacatctggtcccttggcattacttctatagaaatggctgaaggaaaacctccttatgctgatatacat
 201.  V  A  D  I  W  S  L  G  I  T  S  I  E  M  A  E  G  K  P  P  Y  A  D  I  H

 676.  ccaatgagggctatttttatgattcccacaaatccaccaccaacattcagaaagccagaactttggtccgatgat
 226.  P  M  R  A  I  F  M  I  P  T  N  P  P  P  T  F  R  K  P  E  L  W  S  D  D

 751.  ttcaccgattttgttaaaaagtgtttggtgaagaatcctgagcagagagctactgcaacacaacttttacagcat
 251.  F  T  D  F  V  K  K  C  L  V  K  N  P  E  Q  R  A  T  A  T  Q  L  L  Q  H

 826.  ccttttatcaagaatgccaaacctgtatcaatattaagagacctgatcacagaagctatggagatcaaagctaaa
 276.  P  F  I  K  N  A  K  P  V  S  I  L  R  D  L  I  T  E  A  M  E  I  K  A  K

 901.  agacatgacgaacagcaacgagaattggaagaggaagaagaaaattcggatgaagatgagctggattcccacacc
 301.  R  H  D  E  Q  Q  R  E  L  E  E  E  E  E  N  S  D  E  D  E  L  D  S  H  T

 976.  atggtgaagactagtgtgggagagtgtggcaccatgcgggccacaagcacgatgagtgaaggggcccagaccatg
 326.  M  V  K  T  S  V  G  E  C  G  T  M  R  A  T  S  T  M  S  E  G  A  Q  T  M

1051.  attgaacataatagcacgatgttggaatccgacttggggaccatggtgataaacagtgaggatgaggaagaagaa
 351.  I  E  H  N  S  T  M  L  E  S  D  L  G  T  M  V  I  N  S  E  D  E  E  E  E

1126.  gatggaactatgaaaagaaatgcaacctcaccacaagtacaaagaccatctttcatggactactttgataagcaa
 376.  D  G  T  M  K  R  N  A  T  S  P  Q  V  Q  R  P  S  F  M  D  Y  F  D  K  Q

1201.  gacttcaagaataagagtcacgaaaactgtaatcagaacatgcatgaacccttccctatgtccaaaaacgttttt
 401.  D  F  K  N  K  S  H  E  N  C  N  Q  N  M  H  E  P  F  P  M  S  K  N  V  F
```

FIG. 11A

```
1276.  cctgataactggaaagttcctcaagatggagactttgacttttgaaaatctaagtttagaagaactacagatg
 426.  P  D  N  W  K  V  P  Q  D  G  D  F  D  F  L  K  N  L  S  L  E  E  L  Q  M

1351.  cggttaaaagcactggaccccatgatggaacgggagatagaagaacttcgtcagagatacactgcgaaaagacag
 451.  R  L  K  A  L  D  P  M  M  E  R  E  I  E  E  L  R  Q  R  Y  T  A  K  R  Q

1426.  cccattctggatgcgatggatgcaaagaaaagaaggcagcaaaacttt  tga 1476  (SEQ ID NO:1)
 476.  P  I  L  D  A  M  D  A  K  K  R  R  Q  Q  N  F          491  (SEQ ID NO:2)
```

Bold: predicted region of p33/36 in the Krs1 gene product, underline: antigen peptides

FIG. 11B